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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: Mon May 07 13:37:20 EDT 2007

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\*\*\*\*\*

Reviewer Comments:

ErrorCode            ErrorDescription

W213                Artificial or Unknown found in <213> in SEQ ID (6)

E224                <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (6)

Feature <220> and <223> required explaining the source of the genetic material when "Artificial" or "Unknown" are used as the organism.

W213                Artificial or Unknown found in <213> in SEQ ID (7)

E224                <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (7)

Same as above.

W213                Artificial or Unknown found in <213> in SEQ ID (12)

E224                <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (12)

Same as above

W213                Artificial or Unknown found in <213> in SEQ ID (13)

E224                <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (13)

Same as above

W213                Artificial or Unknown found in <213> in SEQ ID (19)

E224                <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (19)

Same as above

W213                Artificial or Unknown found in <213> in SEQ ID (20)

E224                <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (20)

Same as above

W213                Artificial or Unknown found in <213> in SEQ ID (25)

E224                <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (25)

Same as above

W213                    Artificial or Unknown found in <213> in SEQ ID (26)  
E224                    <220>,<223> section required as <213> has Artificial  
sequence or Unknown in SEQID (26)

Same as above

E323                    Invalid/missing amino acid numbering SEQID (11) POS  
(155)

E323                    Invalid/missing amino acid numbering SEQID (11) POS  
(160)

E323                    Invalid/missing amino acid numbering SEQID (11) POS  
(165)

E323                    Invalid/missing amino acid numbering SEQID (11) POS  
(170)

E323                    Invalid/missing amino acid numbering SEQID (11) POS  
(175)

E323                    Invalid/missing amino acid numbering SEQID (11) POS  
(180)

E323                    Invalid/missing amino acid numbering SEQID (11) POS  
(185)

E323                    Invalid/missing amino acid numbering SEQID (11) POS  
(190)

E323                    Invalid/missing amino acid numbering SEQID (11) POS  
(195)

E323                    Invalid/missing amino acid numbering SEQID (11) POS  
(200)

Nubering for SEQ ID # 11 is missing number 155 and number 205 is used  
twice.

\*\*\*\*\*

Application No: 10583785 Version No: 1.0

**Input Set:**

**Output Set:**

**Started:** 2007-05-07 12:52:44.341  
**Finished:** 2007-05-07 12:52:49.535  
**Elapsed:** 0 hr(s) 0 min(s) 5 sec(s) 194 ms  
**Total Warnings:** 8  
**Total Errors:** 18  
**No. of SeqIDs Defined:** 26  
**Actual SeqID Count:** 26

<b>ErrCode</b>	<b>Error Description</b>
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E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (7)
E 323	Invalid/missing amino acid numbering SEQID (11) POS (155)
E 323	Invalid/missing amino acid numbering SEQID (11) POS (160)
E 323	Invalid/missing amino acid numbering SEQID (11) POS (165)
E 323	Invalid/missing amino acid numbering SEQID (11) POS (170)
E 323	Invalid/missing amino acid numbering SEQID (11) POS (175)
E 323	Invalid/missing amino acid numbering SEQID (11) POS (180)
E 323	Invalid/missing amino acid numbering SEQID (11) POS (185)
E 323	Invalid/missing amino acid numbering SEQID (11) POS (190)
E 323	Invalid/missing amino acid numbering SEQID (11) POS (195)
E 323	Invalid/missing amino acid numbering SEQID (11) POS (200)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)

**Input Set:**

**Output Set:**

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<b>ErrCode</b>	<b>Error Description</b>
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (26)

SEQUENCE LISTING

<110> Prof. Dr. Werner Seeger

<120> Novel chimeric plasminogen activators and their pharmaceutical use

<130> 607927-000001

<140> 10583785

<141> 2007-05-07

<150> US/10/583,785

<151> 2006-06-19

<160> 26

<210> 1

<211> 1143

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (1143)

<223> Coding sequence of the surfactant protein B precursor

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Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr

1 5 10 15

ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt 96  
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys  
20 25 30

gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag 144  
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln  
35 40 45

tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga 192  
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly  
50 55 60

gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac 240  
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn  
65 70 75 80

aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg 288  
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu  
85 90 95

gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc 336  
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys  
100 105 110

aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag 384  
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln  
115 120 125

aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa 432  
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys  
130 135 140

tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg 480  
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu  
145 150 155 160

ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc 528  
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu  
165 170 175

gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac 576  
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His  
180 185 190

aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc 624  
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys  
195 200 205

tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag 672  
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys  
210 215 220

ggc gct gta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg 720  
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu  
225 230 235 240

gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc 768  
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile  
245 250 255

ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc 816  
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg  
260 265 270

ctc gtc ctc cgg tgc tcc atg gat gac agc gct ggc cca agg tcg ccg 864  
Leu Val Leu Arg Cys Ser Met Asp Asp Ser Ala Gly Pro Arg Ser Pro  
275 280 285

aca gga gaa tgg ctg ccg cga gac tct gag tgc cac ctc tgc atg tcc 912  
Thr Gly Glu Trp Leu Pro Arg Asp Ser Glu Cys His Leu Cys Met Ser  
290 295 300

gtg acc acc cag gcc ggg aac agc agc gag cag gcc ata cca cag gca 960  
Val Thr Thr Gln Ala Gly Asn Ser Ser Glu Gln Ala Ile Pro Gln Ala  
305 310 315 320

atg ctc cag gcc tgt gtt ggc tcc tgg ctg gac agg gaa aag tgc aag 1008  
Met Leu Gln Ala Cys Val Gly Ser Trp Leu Asp Arg Glu Lys Cys Lys  
325 330 335

caa ttt gtg gag cag cac acg ccc cag ctg ctg acc ctg gtg ccc agg 1056  
Gln Phe Val Glu Gln His Thr Pro Gln Leu Leu Thr Leu Val Pro Arg  
340 345 350

ggc tgg gat gcc cac acc acc tgc cag gcc ctc ggg gtg tgt ggg acc 1104  
Gly Trp Asp Ala His Thr Thr Cys Gln Ala Leu Gly Val Cys Gly Thr  
355 360 365

atg tcc agc cct ctc cag tgt atc cac agc ccc gac ctt 1143  
Met Ser Ser Pro Leu Gln Cys Ile His Ser Pro Asp Leu  
370 375 380

<210> 2  
<211> 837  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1) ... (837)  
<223> Coding sequence of SP-B precursor lacking the C-terminal propeptide

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Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr  
1 5 10 15

ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt 96  
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys  
20 25 30

gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag 144  
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln  
35 40 45

tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga 192  
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly  
50 55 60

gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac 240  
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn  
65 70 75 80

aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg 288  
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu  
85 90 95

gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc 336  
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys  
100 105 110

aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag 384  
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln  
115 120 125

aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa 432  
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys  
130 135 140

tcc	cg	cag	cca	gag	cca	gag	cag	gag	cca	gg	atg	tca	gac	ccc	ctg	480
Ser	Arg	Gln	Pro	Glu	Pro	Glu	Gln	Glu	Pro	Gly	Met	Ser	Asp	Pro	Leu	
145			150			155			160							
ccc	aaa	cct	ctg	cg	gac	cct	ctg	cca	gac	cct	ctg	ctg	gac	aag	ctc	528
Pro	Lys	Pro	Leu	Arg	Asp	Pro	Leu	Pro	Asp	Pro	Leu	Leu	Asp	Lys	Leu	
			165			170			175							
gtc	ctc	cct	gtg	ccc	ggg	gcc	ctc	cag	g	cg	agg	cct	ggg	cct	cac	576
Val	Leu	Pro	Val	Leu	Pro	Gly	Ala	Leu	Gln	Ala	Arg	Pro	Gly	Pro	His	
			180			185			190							
aca	cag	gat	ctc	tcc	gag	cag	caa	ttc	ccc	att	cct	ctc	ccc	tat	tgc	624
Thr	Gln	Asp	Leu	Ser	Glu	Gln	Gln	Phe	Pro	Ile	Pro	Leu	Pro	Tyr	Cys	
			195			200			205							
tgg	ctc	tgc	agg	gct	ctg	atc	aag	cg	atc	caa	gcc	atg	att	ccc	aag	672
Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	Arg	Ile	Gln	Ala	Met	Ile	Pro	Lys	
			210			215			220							
gg	gc	ct	gt	gc	gt	gc	cag	gt	tg	cg	gt	gt	gt	cct	ctg	720
Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln	Val	Cys	Arg	Val	Val	Pro	Leu	
			225			230			235			240				
gt	gc	gg	gc	atc	tgc	cag	tgc	ctg	gct	gag	cg	tac	tcc	gtc	atc	768
Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu	Ala	Glu	Arg	Tyr	Ser	Val	Ile	
			245			250			255							
ct	ctc	gac	ac	ctg	ctg	gg	cg	atg	ctg	ccc	cag	ctg	gtc	tgc	cg	816
Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	Cys	Arg	
			260			265			270							
ctc	gtc	ctc	cg	tg	tcc	atg										837
Leu	Val	Leu	Arg	Cys	Ser	Met										
			275													

<210> 3  
<211> 237  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1) ... (237)  
<223> Coding sequence of the mature surfactant protein B

<400> 3

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Phe	Pro	Ile	Pro	Leu	Pro	Tyr	Cys	Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	
1		5			10			15								
cg	atc	caa	gc	c	at	cc	g	gt	ct	g	cg	ct	gt	gc	gg	96
Arg	Ile	Gln	Ala	Met	Ile	Pro	Lys	Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	
					20			25			30					

cag gtg tgc cgc gtc gta cct ctg gtg gcg ggc atc tgc cag tgc 144  
Gln Val Cys Arg Val Val Pro Leu Val Ala Gly Gly Ile Cys Gln Cys  
35 40 45

ctg gct gag cgc tac tcc gtc atc ctg ctc gac acg ctg ctg ggc cgc 192  
Leu Ala Glu Arg Tyr Ser Val Ile Leu Leu Asp Thr Leu Leu Gly Arg  
50 55 60

atg ctg ccc cag ctg gtc cgc ctc gtc ctc cgg tgc tcc atg 237  
Met Leu Pro Gln Leu Val Cys Arg Leu Val Leu Arg Cys Ser Met  
65 70 75

<210> 4  
<211> 1293  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1) ... (1293)  
<223> Coding sequence of the single-chain urokinase-plasminogen activator

<400> 4

atg aga gcc ctg ctg gcg cgc ctg ctt ctc tgc gtc ctg gtc gtg agc 48  
Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser  
1 5 10 15

gac tcc aaa ggc agc aat gaa ctt cat caa gtt cca tcg aac tgt gac 96  
Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp  
20 25 30

tgt cta aat gga gga aca tgt gtg tcc aac aag tac ttc tcc aac att 144  
Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile  
35 40 45

cac tgg tgc aac tgc cca aag aaa ttc gga ggg cag cac tgt gaa ata 192  
His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile  
50 55 60

gat aag tca aaa acc tgc tat gag ggg aat ggt cac ttt tac cga gga 240  
Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly  
65 70 75 80

aag gcc agc act gac acc atg ggc cgg ccc tgc ctg ccc tgg aac tct 288  
Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser  
85 90 95

gcc act gtc ctt cag cca acg tac cat gcc cac aga tct gat gct ctt 336  
Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu  
100 105 110

cag ctg ggc ctg ggg aaa cat aat tac tgc agg aac cca gac aac cgg 384  
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg  
115 120 125

agg cga ccc tgg tgc tat gtg cag gtg ggc cta aag ccg ctt gtc caa 432  
Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln  
130 135 140

gag tgc atg gtg cat gac tgc gca gat gga aaa aag ccc tcc tct cct 480  
Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro  
145 150 155 160

cca gaa gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc 528  
Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg  
165 170 175

ttt aag att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg 576  
Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp  
180 185 190

ttt gcg gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg 624  
Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val  
195 200 205

tgt gga ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac 672  
Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His  
210 215 220

tgc ttc att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt 720  
Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly  
225 230 235 240

cgc tca agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg 768  
Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val  
245 250 255

gaa aac ctc atc cta cac aag gac tac agc gct gac acg ctt gct cac 816  
Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His  
260 265 270

cac aac gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt 864  
His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys  
275 280 285

gcg cag cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat 912  
Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr  
290 295 300

aac gat ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa 960  
Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys  
305 310 315 320

gag aat tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt 1008  
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val  
325 330 335

gtg aag ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc 1056  
Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly  
340 345 350

tct gaa gtc acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa 1104

Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys  
355 360 365

aca gat tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc 1152  
Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu  
370 375 380

caa ggc cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt 1200  
Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys  
385 390 395 400

gcc ctg aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta 1248  
Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu  
405 410 415

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Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu  
420 425 430

<210> 5  
<211> 828  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1) ... (828)  
<223> Coding sequence of low mw two-chain urokinase-plasminogen activator

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Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys  
1 5 10 15

act ctg agg ccc cgc ttt aag att att ggg gga gaa ttc acc acc atc 96  
Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile  
20 25 30

gag aac cag ccc tgg ttt gcg gcc atc tac agg agg cac cgg ggg ggc 144  
Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly  
35 40 45

tct gtc acc tac gtg tgt gga ggc agc ctc atc agc cct tgc tgg gtg 192  
Ser Val Thr Tyr Val Cys Gly Ser Leu Ile Ser Pro Cys Trp Val  
50 55 60

atc agc gcc aca cac tgc ttc att gat tac cca aag aag gag gac tac 240  
Ile Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr  
65 70 75 80

atc gtc tac ctg ggt cgc tca agg ctt aac tcc aac acg caa ggg gag 288  
Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu  
85 90 95

atg aag ttt gag gtg gaa aac ctc atc cta cac aag gac tac agc gct 336

Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala  
100 105 110

gac acg ctt gct cac cac aac gac att gcc ttg ctg aag atc cgt tcc 384  
Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser  
115 120 125

aag gag ggc agg tgt gcg cag cca tcc cgg act ata cag acc atc tgc 432  
Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys  
130 135 140

ctg ccc tcg atg tat aac gat ccc cag ttt ggc aca agc tgt gag atc 480  
Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile  
145 150 155 160

act ggc ttt gga aaa gag aat tct acc gac tat ctc tat ccg gag cag 528  
Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln  
165 170 175

ctg aaa atg act gtt gtg aag ctg att tcc cac cgg gag tgt cag cag 576  
Leu Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln  
180 185 190